AMENDMENTS TO THE SPECIFICATION:

Please amend this application on page 1, line 1, by inserting the following new paragraph:

This is a division of Application No. 09/644,987, filed August 24, 2000, which claims the benefit of priority of U.S. Provisional Patent Application No. 60/151,074, filed August 27, 1999, all of which are incorporated herein by reference.

Please replace the third full paragraph on page 9, starting on line 15, with the following paragraph:

Figure 1 describes two plasmids of the invention, pHPI 643 (SEQ ID NOS: 3 and 4) and pHPI 644 (SEQ ID NOS: 5 and 6).

Please replace the first full paragraph on page 11, starting on line 3, with the following paragraph:

Figure 4 describes two plasmids of the invention, pHPI 663 (SEQ ID NOS: 7 and 8) and pHPI 668 (SEQ ID NOS: 9 and 10).

Please replace the paragraph bridging pages 14 and 15 with the following paragraph:

Figure 10 (a-f). Potential RNA structures of the wild type and mutated 5' terminus of the HCV RNA (nt1-480) as predicted by the mfold program. The sequence

FINNEGAN
HENDERSON
FARABOW
GARRETT &
DUNNER LLP

1300 I Street, NW
Washington, DC 20005
202.408.4000
Fax 202.408.4400
www.finnegan.com

shown is the consensus sequence for HCV type 1a. The nucleotides of the initiator AUG codon are boxed. Arrows indicate the changes derived from the mutatgenesis experiments. Fig. 10a (SEQ ID NO: 11) wild type sequences present in pHPI643 and pHPI663; Fig. 10b (SEQ ID NO: 12), substitution present in pHPI676; Fig. 10c (SEQ ID NO: 13), substitutions present in pHPI679; Fig. 10d (SEQ ID NO: 14), substitutions present in pHPI1719; Fig. 10e (SEQ ID NO: 15) substitutions present in pHPI720; Fig. 10f (SEQ ID NO: 16) substitution present in pHPI721.

Please replace the first full paragraph on page 15, beginning on line 3, with the following paragraph:

Figure 11 shows the sequence of a polypeptide of the invention in standard single letter abbreviations (amino acids 1 to 161 of SEQ ID NO: 1) designated herein as "core+1 protein", and its relationship to the core gene of HCV. The amino acids in bold type designate amino acids present in the catalytic site of the papain-like proteases.

Please replace the second full paragraph on page 15, beginning on line 9, with the following paragraph:

Figure 12 contains the nucleotide sequence of core+1 DNA (SEQ ID NO: 2) and the amino acid sequence of core+1 protein (SEQ ID NO: 1). Specifically, the first line in Figure [11] 12 is the nucleotide sequence of the coding strand, second line is the

FINNEGAN
HENDERSON
FARABOW
GARRETT &
DUNNER LLP

1300 I Street, NW
Washington, DC 20005
202.408.4000
Fax 202.408.4400
www.finnegan.com

nucleotide sequence of the complementary strand, the third line is the amino acid sequence of the novel polypeptide, and the fourth line is produced by the computer program (McVector). A putative "slippery site(s)" and/or novel RNA signal(s) is identified between nucleotides 345 and 460.

Please replace the paragraph bridging pages 38 and 39 with the following paragraph:

As a first step the nucleotide sequence 350-1054 was cloned into the pmal-c2 expression vector, resulting in plasmid pHPI 643 (Figure 1; panel A (SEQ ID NOS: 3 and 4)). Sequencing of this plasmid confirmed the correct frame between the maltose-binding protein and core+1. The fused malE-core+1(L) protein had a calculated MW of ~60 kDa.

Please replace the paragraph bridging pages 39 and 40 with the following paragraph:

Taken together, these results indicate that 1) the pHPI 643 plasmid (SEQ ID NO: 3) produces a protein (SEQ ID NO: 4) that is recognized by the HCV-positive human serum and 2) the majority of the recombinant protein is degraded or specifically cleaved near the fusion site resulting in the apparent discrepancies between the calculated and apparent MW of the protein.

FINNEGAN
HENDERSON
FARABOW
GARRETT &
DUNNER LLP

1300 I Street, NW
Washington, DC 20005
202.408.4000
Fax 202.408.4400
www.finnegan.com

Please replace the first full paragraph on page 40 with the following paragraph:

In an effort to overcome the degradation/processing or specific cleavage of the fusion protein, a second plasmid was constructed (pHPI 644) (Figure 1; panel B (SEQ ID NOS: 5 and 6)), which was designed to produce a malE-core+1(S) fusion protein truncated by 13 aa at the amino terminus of the putative core+1 protein. The reason for this deletion was to avoid sequences of the amino terminal region of the core gene, which were suspected to have an effect on the stability of the protein.

Please replace the first paragraph on page 42, beginning on line 2, with the following paragraph:

To test whether the problem with the differences in the MW was related to the properties of the pmal-c2 expression vector, two additional core+1 chimeric proteins were produced using the pGEX-3x expression vector. Plasmid pHPI 663 contains nt 345-774 from the core coding region (Figure 4; panel A (SEQ ID NOS: 7 and 8)) and produces a GST-core+1(L) recombinant protein with a calculated MW of 41 kDa. Plasmid pHPI 668 contains nt 390-920 from the core coding region and produces a GST-core+1(S) recombinant protein truncated by 9 amino acids at the amino terminal of core+1 with regard to pHPI 663 (Figure 4; panel B (SEQ ID NOS: 9 and 10)). This truncated GST-core+1(S) protein has a calculated MW of 41 kDa. Sequencing of both plasmids confirmed the correct frame between the glutathione-S-transferase and core+1 protein.

FINNEGAN
HENDERSON
FARABOW
GARRETT &
DUNNER LLP

1300 I Street, NW
Washington, DC 20005
202.408.4000
Fax 202.408.4400
www.finnegan.com

Please replace the first paragraph on page 48, beginning on line 1, with the following paragraph:

In an attempt to analyze these data, we examined the secondary RNA structure of nt 342-830 by the MFOLD program. As shown in Figure 10a (SEQ ID NO: 11), this program predicts an extensive secondary structure within this region. Interestingly, mut R1, mut R2, and mut R3 (Figure 10b (SEQ ID NO: 12), 10c (SEQ ID NO: 13), and 10d (SEQ ID NO: 14)) predict minimum changes in the RNA secondary structure, whereas mut R4 and mut R5 are predicted to cause a rather severe effect on the RNA folding pattern (Figures 10e (SEQ ID NO: 15) and 10f (SEQ ID NO: 16)). Thus, there appears to be a rather direct correlation between the RNA secondary structure and the synthesis of the core-related 30 kDa protein band.

Please associate the Sequence Listing filed herewith at the end of the Specification.

FINNEGAN
HENDERSON
FARABOW
GARRETT &
DUNNER LLP

1300 I Street, NW
Washington, DC 20005
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www.finnegan.com